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Best Local Similarity 100.0
Matches 557; Conservative
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Q28006 bom sapien
Q28006 bom sapien
Q28006 bom sapien
Q9nu91 homo sapien
Q9nu91 homo sapien
Q9nsn7 homo sapien
Q9nsn7 homo sapien
Q9ng strongyloce
Q8cew8 homo sapien
Q9uc79 strongyloce
Q8cew8 homo sapien
Q9smx7 homo sapien
Q9smx7 homo sapien
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Q8cfl1 mus musculu
                                                                                                                                                                 October 9, 2003, 10:57:41; Search time 37.6351 Seconds (without alignments) 3819.179 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                   1 MSDGTASARSSSPLDRDPAF........SCAEESEEDCPRELTDPKS 557
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                   - protein search, using sw model
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QB1VZ5
Q29M33
Q28M34
Q29M34
Q39M34
Q35889
Q36M6
Q36M6
Q36M6
Q36M6
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1: Sp_archea:*
2: Sp_bacteria:*
3: Sp_tungi:*
4: Sp_human:*
5: Sp_mammal:*
5: Sp_mammal:*
5: Sp_mammal:*
5: Sp_phage:*
5: Sp_ph
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Q96NX7
Q8IUC7
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sp_rvirus:*
sp_bacteriap:*
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sp_virus:*
sp_vertebrate:*
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Maximum DB seq length: 200000000
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Indels

100.0%; Score 2832; DB 11; Length 557; 100.0%; Pred. No. 1.1e-157; ive 0; Mismatches 0; Indels 0;

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946112 drosophila

965412 mus musculu

95646 caenorhabdi

95666 caenorhabdi

95666 caenorhabdi

967402 mus musculu

99659 drosophila

99738 ustilago ma

98738 ustilago ma

98675 homo sapien

96675 homo sapien

96755 homo sapien

96755 homo sapien

99765 homo sapien

99765 homo sapien

99743 drosophila

9975 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9bic1 caenorhabdi
Q9xy66 caenorhabdi
Q9vqm0 drosophila
Q8r1d2 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus. NCBL_TaxID=10090;
              Q9hg12
Q9w3v2
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
Syntaxin4-interacting protein synip.
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Q62402
Q9V6P9
P87198
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Q8R1D2
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Q8IR55
Q8IPZ1
Q8IPZ2
Q8MRI5
            Q9HGL2
Q9W3V2
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Q81R54
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC041485; AAH41485.1; -.
SEQUENCE 245 AA; 26974 MW; 4E92DDBBFD27DF79 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to syntaxin binding protein 4.
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Matches 165, Conservative
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                                                                                  DGRLKPGDQLVSINKESMIGVSFBEAKSIITRAKLRSESPWEIAFIRQKSYCGHPGNICC 120
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                    DGRLKFGDQLVSINKESMIGVSFEBAKSIITRAKLRSESPWEIAFIRQKSYCGHPGNICC
                                                                                                                                                                                              PSPQVSEDCGPQTSTFTLLSSPSETLLPKTSSTPQTQDSTFPSCKAIQTKPEHDKTEHSP
                                                                                                                                                                                                                                                                                 EALREQVQADSKGTVSFGDFVQVARSLFCLQLDEVNVGVHEIPSILDSQLLPCDSLEADE
                                                                                                                                                                                                                                                                                                                                                                             EALREQUQADSKGTVSFGDFVQVARSLFCLQLDEVNVGVHEIPSILDSQLLPCDSLEADE
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                                                                                                                                                                       PSPQVSEDCGPQTSTFTLLSSPSETLLPKTSSTPQTQDSTFPSCKAIQTKPEHDKTEHSP
                                                                                                                                                                                                                                                          ITSLDNSPADTSNADIAPAWTDDDSGPQGKISLNPSVRLKAEKLEMALNYLGIQPTKEQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EAAQRQAHGMEMDYBEVIRLLEAEVSELKAQLADYSDQNKESVQDLRKRVTVLDCQLRKS
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OBCELI;
OBCELI;
OLIMAR.2003 (TERBLEI. 23, Created)
OL-MAR.2003 (TERBLEI. 23, Last sequence update)
OL-MAR.2003 (TERBLEI. 23, Last annotation update)
OLIMAR.2003 (TERBLEI. 23, Last annotation update)
Similar to syntaxin binding protein 4.
Mus musculus (Mouse)
Eukaryoca, Meracaa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muxinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC032881; AAH32881.1; -.
SEQUENCE 533 AA; 58591 MW; 8B6BC19511E3AF09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.1%; Score 2522; DB 11;
larity 100.0%; Pred. No. 1.4e-139;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEESEEDCPRELTDPKS 557
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SEQUENCE FROM N.A.
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Best Local Simil
Matches 501;
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Q8CFL1
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1141 PQETVIRELQPQQQPRTIERRDLQYITVSKEELSS-----GDSLSPDP----WKRD 1187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1395 TAKFVAYN---EEEEEEDC--SLAGPNS 1417
                                                                                                                                                                                                                                                                                                                                                                                                                                      530 HPVMSALNLSCAEESERDCPRELTDPKS 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BA14 tyrosine phosphatase (EC 3.1.3.48).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR000387; TYR phosphatase.
InterPro; IPR000317; Band 41; I.
Pfam; PF00102; Y phosphatase; I.
Pfam; PF00102; Y phosphatase; I.
PRINTS; PR0035; BAND41.
PRINTS; PR00700; PRTYPHPHTASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1081 EEHQRWYEKEKARLEEERERKRREQERKLGGMRTQSLNPAPFSPLTAQQMKPEKPSTLQR 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .021 PVAVSQPIRTDLPPPPPPPPWHYAGDFDGMSMDLPLPPPPSANOIGLPSAQVAAABRRKR 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 -----TSLDNSPA----DISNADIAPAWTDDDSGPQGK----- 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             666 AQPLRKEPELITUTLKKQNGMGLSIVAAKGAGQDKLGIYVKSVVKGGAADVDGRLAAGDO 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:|:: |::|:|| ::|| |:|| |:|| |:|| ::|| |:|| ::|| |:|| ::|| |:|| ::|| |:|| ::|| |:|| ::|| |:|| ::|| |:|| ::|| |:|| ::|| |:|| ::|| |:|| ::|| |:|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVSINKESMIGVSFEEAKSIITRAKLRSESPWEIAFIRQKS-YCGHPGNICCPSP---QV 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  902 PASKSODRMAPPONOWPNYEEKPHMHTDSNHSSIAIQRVTRSQEELREDKAYQLERHRIE 961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     782 SDRRGSGKPRPKSEGFELYNNSTONGSPESPOLPWAEYSBPKKLPGDDRLMKNRADHRSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 SSPLDRDPAFRVITVTKETGLGLKILGGINRNEGPL-VYIHEVIPGGDCYKDGRLKPGDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 -ISLNPSVR------LKAEKLEMAL-----NYLGIQPT-----
                                                                                                              01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 15, Last annotation update)
01-0AR-2003 (TrEMBLrel. 2) Last annotation update)
DJ470B24.1.5 (Myeloid/lymphoid or mixed-lineage leukemia (Trithorax (Drosophila) homolog), translocated to, 4 (AF-6) (Isoform 5))
                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.9%; Score 195.5; DB 4; Length 1492; Best Local Similarity 18.8%; Pred. No. 0.0049; Matches 152; Conservative 103; Mismatches 236; Indels 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 PSCKA------IQTKPE-HDKTEHSPI-------
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Williams S.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 PDZ/DHR DOWAIN.
EMBL, AL049698; CAB76849.1; -.
HISSP: Q12923; 3PDZ.
HISSP: Q12923; 3PDZ.
InterPro; IPR007710; DIL.
InterPro; IPR007710; DIL.
InterPro; IPR001478; PDZ.
IpterPro; IPR00478; FHA.
IpterPro; IPR00498; FHA.; I.
Pfam; PF00595; PDZ; I.
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SEQUENCE 1492 AA; 168511 MW; 80207118EF0419BF CRC64;
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                                                                          PRT; 1492 AA
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SMART; SM00228; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                        (Fragment).
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1188 A-----KEKL---EKQQQMHIVDMLSKEIQELQSKPDRSAEESDRLRKLMLEWQFQK 1236
                                                                                                                                                                                                                                                                                                           1336 HDEAARRLLE-PRAPGLCRPPLPRDYEPPSPSPAPGAPPPPPPQRNASYLKTQVLSPDSLF 1394
                                                                                                                                                                                                                           358 HLAEAAQRQAHGMEMDYEEV--IRLLEAEVSELKAQLADYSDQNKESVQDLRKRVTVLDC 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         476 RSFPATLLLESKELVRSVRAILDMDCLPYGWEEAYTAD-----GIKYFINHVTQTTSWI 529
310 AALEERNVLKEKLLESEKHRK----QLIEELQNVKQEAKAVAEETRALRSRI----- 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                              416 QLRKSEMARKAFKASTERLLGFIEAIQEVILDSSAPLSTLSERRAVLASQTSLPLLARNG 475
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Vega Q.C., Walton K.M., Dixon J.E.;

Vega Q.C., Walton K.M., Dixon J.E.;

Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.

-!- CATALYTIC ACTIVITY:

TYROSINE + PHOSPHATE.

-!- SIMILARITY: CONTAINS A DOMAIN FOUND IN BAND 4.1, EZZIN, MOESIN,

RADIXIN, AND TALIN.

-!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-

FYROSINE PHOSPHATASE FAMILY.

EMBL; U20801; AAA73516.1; -.

EMBL; U208029; BADZ.

InterPro; IPR002299; Band 4.1.
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00255, B41; 1.

SMART; SM00258; B02; 5.

SMART; SM00124; PTPC; 5.

RROSITE; PS00661; BAND 41_2; FALSE NEG.

RROSITE; PS50061; BAND 41_2; FALSE NEG.

RROSITE; PS50051; BAND 41_3; 1.

RROSITE; PS500183; TYR PHOSPHATASE 1; FALSE NEG.

RROSITE; PS50056; TYR PHOSPHATASE 2; 1.

RROSITE; PS50056; TYR PHOSPHATASE PPP; 1.

RROSITE; PS50055; TYR PHOSPHATASE PPP; 1.

RROSITE; PS50056; TYR PHOSPHATASE PPP; 1.
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BY SIMILARITY.
COILED COIL (POTENTIAL).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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961 AAMDRKSDSDMWINQSSSLDSSTSSQEHLNHSSKSVTPASTLTKSGP-GRWKTPAALPAT 1019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVSINKESMIGVSFERAKSIITRAKLRSESPWEIAFIRÇKS-YCGHPGNICCPSP---QV 125
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                                                                                                                                                                                                                                                                                                                                                                                                                       11 SSPLDRDPAFRVITVTKETGLGLKILGGINRNEGFL-VYIHEVIPGGDCYKDGRLKPGDQ
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                                                                                                                                                                                                                                                                                                                          Length 1427;
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Last annotation update)
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                                                                                                  Pfam; PF01843; DIL; 1.
Pfam; PF00499; FHA; 1.
Pfam; PF00595; PDZ; 1.
SMART; SM00240; FHA; 1.
SMART; SM00228; PDZ; 1.
PROSITE; PSS0106; PDZ; 1.
HSSP; Q12923; srue.
InterPro; IPRO02710; DIL.
InterPro; IPRO0253; FHA.
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                                                                                                                                                                                                                                                                         ------ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 FPSCKAIOTKPEHDKTEHSPITSLDNSPADTSNADIAPA------WTDDDS----GP 207
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                                                                                                                                                                            68
                                                                                                                                                                       10 SSSPLDRDPAFRVITVTKETGLGLKILGGINRNEGPL-VYIHEVIPGGDCYKDGRLKPGD
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2009 (TrEMBLrel. 24, Last annotation update)
(Drosophila) homolog), translocated to, 4 (AF-6) (Isoform 4))
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                                                                        Query Match 6.8%; Score 192.5; DB 6; Length 2484; Best Local Similarity 22.8%; Pred. No. 0.014; Matches 142; Conservative 79; Mismatches 253; Indels 149;
                                                                                                                                                                                                                                                                       QLVSINKESMIGVSFEEAKSIITRAKLRSESPWEIAFI------
     COILED COIL (POTENTIAL).
276382 MW; 45A92F0D4F1ED13D CRC64;
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Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
EMBL; AL049698; CAB76848.1; -.
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     1793
     1761 179
2484 AA;
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1249 EEE------EDDDVDTMLIMQRLEABRR---ARQTAMPAIS 1280
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                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00240; FHA; I. SMART; SM00228; PDZ; I. SMART; SM00314; RA; 2.
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Best Local Similarity
Matches 118. Comment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----VIRLLEAEVSELKAQLADYSDQNKESVQDLRKRVTVLDCQLRKSEMARKAFKA 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     666 AQPLRKEPEIITVTLKKQNGMGLSIVAAKGAGQDKLGIYVKSVVKGGAADVDGRLAAGDQ 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 LVSINKESMIGVSFERAKSIITRAKLRSESPWEIAFIRQKS-YCGHPGNICCPSP---QV 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ...... 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------QGKISLNPSVRLKAEKLE 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 -----10DSTFPSCKAIQTKPEHDKTEHSPITSLDNS---- 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 842 PNVANQPPSPGGKSAYASGTTAKITSVSTGNLCTEEQTPPPRPEAYPIPTQTYTREYFTF 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 SSPLDRDPAFRVITVTKETGLGLKILGGINRNEGPL-VYIHEVIPGGDCYKDGRLKPGDQ 69
DJ470B24.1.2 (Myeloid/lymphoid or mixed-lineage leukemia (Trithorax (Drosophila) homolog), translocated to, 4 (AF-6) (Isoform 2)) (Fragment).
                                                                                                                                                                             Eukaryofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.5%; Score 183.5; DB 4; Length 1333; Best Local Similarity 18.6%; Pred. No. 0.021; Matches 120; Conservative 104; Mismatches 209; Indel8 211;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 1333 AA; 150861 MW; 691F95FA834D1AA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                  Williams S.;
Submitted (PEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
EMBL; AL049698; CAB76851.1; -..
HSSP; Q12923; 3PDZ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro, IPR002710; DIL.
Interpro, IPR000253; FHA.
Interpro, IPR001478; PDZ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00240; FHA; 1.
SMART; SM00228; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01843; DIL; 1.
Pfam; PF00498; FHA; 1.
Pfam; PF00595; PDZ; 1.
                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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1005 TQPLRKEPEVITVTLKKQNGMSLSIVAAKGAGQDKLGIYVKSVVKGGAADVDGRLAAGDQ 1064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1181 PNVANQPPSPGGKSPYTSGTAAKITSVSTGNLCTEEQTPPPRPEAYPIPTQTYTREYFTF 1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |: |:
|: PASKSQDRMAPVQNQWPNYEEKPHMHTESDHASIAIQRVTRSQBELREEKVYQLERHRVE 1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1360 PVAVSQPIRTDLPPPPPPPPAHYTSDFDGISMDLPLPPPPANQAAPQSAQVAAAERKKRB 1419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lery Match 6.5%; Score 183; DB 11; Length 1829;
st Local Similarity 17.8%; Pred, No. 0.034;
tches 118; Conservative 108; Mismatches 160; Indels 278; Gaps
                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=97477397; PubMed=9334353;
Mandai K., Nakanishi H., Satoh A., Obaishi H., Wada M., Nishioka H.,
Itoh M., Mizoguchi A., Aoki T., Fujimoto T., Matsuda Y., Tsukita S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takai Y.;
A novel actin filament-binding protein with one PDZ domain
localized at cadherin-based cell-to-cell adherens junction.";
J. Cell Biol. 139:517-528(1997).
-:-SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50106; PDZ; 1.
SEQUENCE 1829 AA; 207676 MW; 45CS97A82F109D6F CRC64;
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01-07N-1998 (TrEMBLrel. 05, Created)
01-07N-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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InterPro; IPR00253; FHA.
InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
Pfam; PF01843; DIL; 1.
Pfam; PF00498; PHA; 1.
Pfam; PF00595; PDZ; 1.
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LUSINKESMIGUSFEEAKSIITRAKLRSESPWEIAFIRQKS-YCGHPGNICCPSP---QV 125
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                                                                                                                            277 VGVHEIPSILDSQLLPCDSLEAD-----EVGKLRQERNAALEERNVLKEKLLESEKHRK 330
                                                                                                                                                                                                  331 QLIEELQNVKQEAKAVAEETRALRSRIHLAEAAQRQAHGMEMDYEEVIRLLEAEVSELKA 390
                                                                                                                                                                                                                                      681 KNLEBLFQVKMEREQHQTE1RDLQDQL-----SEM-HDELDSAKRSEDRE-KG 726
                                                                                                                                                                                                                                                                                                            727 ALIEELLOAKODLODLLIAKEEQEDLLRKRERELTÄLKGALKEEVSSHDQEMDKLKEQYD 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 SSPLDRDPAFRVITVTKETGLGLKILGGINRNEGPL-VYIHEVIPGGDCYKDGRLKPGDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               664 AQPLRKEPEIITVTLKKQNGMGLSIVAAKGAGQDKLGIYVKSVVKGGAADVDGKLAAGDQ
                   ---PDSGAK-KISVKTFPSASNTQATPDLLKGQQELTQQTNEETAKQILYN
                                                                                                                                                   QLADYSDQNKESVQDLRKRVTVLDCQLRKSEMARKAFK-ASTERLLGFIEAIQEVLLDSS
                                                                                                                                                                                                                                                                                                                                                 450 APLSTLSE-----SKELVRSV-SQTSLPLLARNGRSFPATLLLE-----SKELVRSV-
                                                                                         562 YLKEGSTDNDDATKRKVNLVFEKIQTLKSRAAGSAQGNNQACNSTSEVKDLL-EQKSKLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cuery Match 6.4%; Score 181.5; DB 4; Length 1410; Best Local Similarity 17.6%; Pred. No. 0.03; Matches 121; Conservative 97; Mismatches 175; Indels 295; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ansorge W., Wirkner U., Mewes H.W., Weil B., Wiemann S., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-! SINILIARITY: CONTAINS 1 PDZ/DHR DOMAIN.
EMBL: ALIALIST3: CABA2312.1; -.
HSSP; Q12923; 3PDZ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                     494 --- RAILDMDCLPYGWEEAYTADGIKYFINHVTQ 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                          847 QLQRQIEDLK----GDEAKAKETLKKFEGEIRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last seqt
01-MAR-2003 (TrEMBLrel. 23, Last ann
Hypothetical protein (Fragment).
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InterPro: IPR002710; DIL.
InterPro: IPR00183; FHA.
InterPro: IPR001479; PPEam; PF004849; FHA; 1.
Pfam; PF004949; FHA; 1.
Pfam; PR002595; PDZ; 1.
SMART; SM00240; FHA; 1.
PR0SITE; PS50106; PDZ; 1.
Hypothetical protein.
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513 TS-
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                         1519 DPWKRDAREKLEKOCOMHIVDMLSKEIHELQNKGDRTAEESDRLRKLMLEWOFOKRLOES 1578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            397 ---LQGNSEYLIEFSRNLGKSSEHLLRPSQVCPQRPLSQERRGKQSVGRTFAKLQGAAHG 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----PSETLLPKTSSTPQTQDSTF---PSCKAIQTKPEHDKTEHSPITSLDNSPAD 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    454 ASCAHSRPPOPNIDGKVLETEGSQESTVIRAPSLGAQSKKEEEVKTATATL-MLQNRAAA 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 TSNADIAPAWTDDDSGPQGKISLN--PSVR-----LKAEK-----LEMALN 229
                                                                         277 VGVHEIPSILDSQLLPCDSLEADEVGKLR-QERNAALEERN-----VLKEKLLES---- 325
   LNYLGIQPTK----EQREALRE-----QVQADSKGTVSFGDFVQVARSLFCLQLDEVN 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91
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                                                                                               -----EKHRKO------LIBELQNVKQEAKAVAEETRALRSRI------HLAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 --GPLVYIHEVI----PG----GDCYKDGRLKPGDQLVSINKESMIGVSFBEAKSIIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346 DTGSIPGVDQLIEKFDQKPGLQRRGRSGKRNRINPDDRKRSRSVDSAPPFG-----
                                                                                                                                                                                                                     AQRQAHGMEMDYEEV -- IRLLEAEVSELKAQLADYSDQNKESVQDLRKRVTVLDCQLRKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ3111 (Fragment).
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.4%; Score 182.5; DB 4; Length 883; 22.6%; Pred. No. 0.015; tive 87; Mismatches 245; Indels 159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "NEDO human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AX056673; BAB71249.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     883 AA; 99335 MW; 5D797322EA4BB467 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         883 AA
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NON TER 883 86
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Matches
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1076 ERRKRBEHORWYEKEKARLEEERERKRREQERKLGOMRTOSLNPAPFSPLTAQOMKPEKP 1135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1022 VAVSQPIRTDLPPPPPPPPPPVHYAGDFDGMSMDLPLPPPPPSANQIG----LPS---AQVAAA 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257 -----VGVH5IPSILDSQLLPC 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 LESEKHRKQLIBELQNVKQEAKAVAEETRALR----SRIHLAEAAQRQAHGMEMDYEE-- 376
                                                                                                                                                                                                                                                                                                                                 666 AQPLRKEPBIITVTLKKQNGMGLSIVAAKGAGQDKLGIYVKSVVKGGAADVDGRLAAGDQ 725
                                                                                                                                                                                                                                                                                                    LVSINKESMIGVSFEEAKSIITRAKLRSESPWEIAFIRQKS-YCGHPGNICCPSP---QV 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 -----1QDSTFPSCKAIQTKPEHDKTEHSPITSLDNS---- 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1193 EKQQQMHIVDMLSKEIQELQSK----PDRSAEESDRLRKIMLEWQFÇKRLQESKQK 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         842 PNVANQPPSPGGKSAYASGTTAKITSVSTGNLCTEEQTPPPRPEAYPIPTQTYTREYFTF
                                                                                                                                                                                            11 SSPLDRDPAFRVITVTKETGLGLKILGGINRNEGPL-VYIHEVIPGGJCYKDGRLKPGDQ
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97477397; PubMed=9334353;
Mandai K., Nakanishi H., Satoh A., Obaishi H., Wada M., Nishioka H.,
Itoh M., Mizoguchi A., Aoki T., Fujimoto T., Matsuda Y., Tsukita S.,
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                                                                        6.3%; Score 178; DB 4; Length 1296;
18.5%; Pred. No. 0.043;
tive 94; Mismatches 194; Indels 198;
  1
1296 AA; 145808 MW; 9FECCF3CA67D19EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               126 SEDCG----PQTSTFTLLSSPSETLLPKTSSTPQ------
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Last annotation update)
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                                                                                                        Best_Local Similarity 18.5%
Matches 110; Conservative
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NON TER
SEQUENCE
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                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                           960 AAMDRKSDSDMWINQSSSLDSSTSSQEHLNHSSKSVTPASTLTKSGP-GRWKTPAAIPAT 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1196 MHIVD--------MLSKEIQELQSKPDRSAEBSDRLRKLMLBWQFQKRLQES 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (019 PVAVSQPIRTDLPPPPPPPPVHYAGDFDGMSMDLPLPPPPSANQIGLPSAQVAAABRRKR 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 -----QVARSLFCLQLDEVNVGVHEIPSILDSQLLPCDSLEADEVGKLRQERN 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 AALEERNVLKEKLLESEKHRKOLIBELONVKOEAKAVAEETRALRSRI-----HLAEA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 AQRQAHGMEMDYEE-----VIRLLEAEVSELKAQ-----LADYSDQNKESVQD 405
                                                            900 PASKSODRMAPPONOWPNYEEKPHMHTDSNHSSIAIORVTRSOEELREDKAYOLERHRIE 959
                                                                                                                                                                                                                                                                                                                                                        ------TSLDNSPA----DISNADIAPAWIDDDSGPQGK----- 210
                                                                                                                                                                                         840 PNVANOPPSPGGKSAYASGTTAKITSVSTGNLCTEEQTPPPRPEAYPIPTQTYTREYFTF 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237 ------KEQREALRE-----QVQADSKGTVSFGDFV-----
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2011 (Myeloid/lymphoid or mixed-lineage leukemia (Trithorax (Drosophila) homolog), translocated to, 4 (AF-6) (Isoform 1))
(Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 -ISLNPSVR-----NYLGIQPT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Williams S.;
Submitted (FEB-2000) to the BMBL/GenBank/DDBJ databases.
Submitted (FEB-2000) to the BMBL/GenBank/DDBJ databases.
SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
EMBL, AL049698; CAB76852.1;
HSSP; Q12923; 3PDZ.
InterPro; IPR000210; DIL.
InterPro; IPR000253; FHA.
InterPro; IPR0001478; PDZ.
                          126 SEDCG----PQTSTFTLLSSPSETLLPKTSSTPQTODS----
                                                                                                                                                                                                                                             162 PSCKA-----IQTKPE-HDKTEHSPI----
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1296 MRKREA--EDRARQEEERRRQEEERTKR 1321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01843; DIL; 1.
Pfam; PF00498; FHA; 1.
Pfam; PP00595; PDZ; 1.
SWART; SW00240; FHA; 1.
SWART; SW00228; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
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PRT; 1136 AA
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Strongylocentrotus
NCBI_TaxID=7668;
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Q8TEW8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1294 SGMDRKCDSDMMINQSSSVESSTSSQEHLNHSSKSVTPASTLTKSGPGRWKTPAAVLPTP 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1234 PASKSODRMAPVONOWPNYBEKPHMHTESDHASIAIORVTRSOEELREEKVYOLERHRVE 1293
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Kinesin-C.
Strongylocentrotus purpuratus (Purple sea urchin).
Bukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea; Euchinoidea; Echinocen; Echinoide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVSINKESMIGVSFEEAKSIITRAKIRSESPWEIAFIROKS-YCGHPGNICCPSP---QV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1354 VAVSQPIRTDLPPPPPPPPPHYTSDFDGISMDL-PLPPPPANQAAPQSAQVAAAERKKRE
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                                                                                                                                                                                                                                                                                                                                                                                              11 SSPLDRDPAFRVITVTKETGLGLKILGGINRNEGPL-VYIHEVIPGGDCYKDGRLKPGDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PADTSNADIAPA---WTDDDSGP------QGKISLNPSVRLKAEKLE
                                                                                                                                                                                                                                                                                               Similarity 19.6%; Pred. No. 0.063; 26; Conservative 93; Mismatches 214; Indels 209; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MALN-----YLGIQPTKEQREALREQVQADSKGTVSFGDF------
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                                                                                                                                                                                                                                                     188980 MW; 65C54B0ED2D0C74C CRC64;
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InterPro; IPR000253; FHA.
InterPro; IPR001478; PDZ.
InterPro; IPR000159; RA_domain.
                                                                                                                                                                                                                                                                                                                                              Matches 126; Conservative
                                                           Pfam; PF01843; DIL; 1.
Pfam; PF01843; EHA; 1.
Pfam; PF00498; FD2; 1.
Pfam; PF00788; RA; 2.
SMART; SM02240; FHA; 1.
SMART; SM01240; FHA; 1.
SMART; SM01349; PD2; 1.
PF0SITE; PS50106; PDZ; 1.
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                                                                                                                                                                                                                                                        1663 AA;
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969 IEALBOEKLONIPPDTAKEINSLYNKVKELERQRDAAQKEAIAKTAEASKINVDFSSTQK 1028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------VQDLRKRVTVLDCQLRKSEM-ARKA--FKASTERLLGFIEAIQEVL 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 QPTKEQREALREQVQ------ADSKGTVSFGDFVQVARSLFCLQLDEVNVGVHE 281
**ROGER'S CO. Hart C.L. Wedaman K.P., Scholey J.M.;

**ROGER'S C.C. Hart C.L. Wedaman K.P., Scholey J.M.;

**Interification of Kinesin-C., a calmodulin-binding carboxy-terminal Kinesin in animal (Strongylocentrotus purpuratus) cells.";

**J. Mol. Biol. 294:1-8(1999).**

**InterPro's Linesin motor.**

**REMBL'S PRO0380; Kinesin motor.**

**REMBL'S PRO0380; Kinesin i. ...

**REMBL'S PRO0380; Kinesin i. ...

**REMBL'S PRO0380; Kinesin motor.**

**REMBL'S PRO0380; Kinesin motor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 LKPGDQLVSINKESMI-----GVSFEBAKSIITRAKLRSESPWEIAFIRQKSYCGHPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             796 GGGGDGGVSSEEMEELQARITELEEENESLTDSTRELEETKEDMEEKIEDLKARIKELEE
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Partitioning-defective 3-like protein splice variant
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Job time : 44.6351 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              741 GA-LNCESAPQGNSELE-DMENKARK------VKKTKEKEKKKEKGKLKVKEKKRKE 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3: | | 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 SSPSETLLPKTSSTP--QTQDSTFPSCKAIQTKPEHDKTEHSPITSLDNSPADTSNADIA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            683 YFPDQHINFR-SVTPARQPESINLKASKSMDLVPDESKV-HSLAGQKSEGLSDKSSHSGQ 740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                790 ENEDPERKIKKKGFGAMLR-----FGKKKE 814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 GLGLKILGGINRNEGP--LVYIHEVIPGGDCYKDGRLKPGDQLVSINKESMIGVSFEEAK 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             568 ETLRRSMSMEGNIRGMIQLVILRRPBRPME----DPAECGAFSKPCFENCQNAVTTSRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.1%; Score 174; DB 4; Length 1136;
19.9%; Pred. No. 0.063;
tive 59; Mismatches 130; Indels 154; Gaps
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SEQUENCE FROM N.A.
Gao L., Macara I.G., Joberty G.;
"Multiple splice variants of Par3 and of a novel related gene, Par3L,
                                                                                                                                                                                                      gene, PAR3L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Partitioning-defective 3-like protein splice variant
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858 ARGL-LDY 864
                          Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 TSTFTLLSSPSETLLPKTSSTPQTQDS--TFPSCKAIQTKPEHDKTEHSPITSLDNSPAD 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                508 GLGVSLKGNKSRETGTDLGIFIKSIIHGGAAFKDGRLRMNDQLIAVNGBSLLGKSNHBAM 567
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                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                     151;
                                                                                                                                                                                                                                                                                                                            Length 1205;
produce functionally different proteins.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARIUS: COMPAINS 3 PDZ/DHR DOMAINS.
EMBL; AF428250; AAL30664.1; -.
Genew; HGNC:14446; AL52CR19.
InterPro; IRR01474; PDZ.
Ffam; PF00595; PDZ; 3.
SMART; SM00228; PDZ; 3.
SRART; SM00228; PDZ; 3.
SROGTTE; PSS106; PDZ; 3.
SEQUENCE 1205 AA; 132494 MM; 26E6704CCDCE8CD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||||::||| :::|| EELEKWKEERRERIGAKHQELR------EKQARGL-LDY 933
                                                                                                                                                                                                                                                                                                                         6.1%; Score 171.5; DB 4;
20.4%; Pred. No. 0.095;
vative 70; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284 SILDSQLLPCDSLEADEV-------
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                                                                                                                                                                                                                                                                                                                                                       Local Similarity 20.4% nes 94; Conservative
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Sequence 13, Appl Sequence 13, Appl Sequence 131, Appl Sequence 151, App Sequence 151, App Sequence 151, App Sequence 1314, App Sequence 1314, App Sequence 1314, App Sequence 13175, App Sequence 1311, App Sequence 1311
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Sequence 48, Appl
Sequence 2, Appli
Sequence 1, Appli
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Sequence 8240, Ap
Sequence 23564, A
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TITLE OF INVENTION: Gene Encoding Syntaxin Interacting Protein
FILE REFERENCE: 09/647,976
CURRENT APPLICATION NUMBER: US/09/647,976A
CURRENT FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: PCT/US99/08568
PRIOR PILING DATE: 1999-04-19
PRIOR PILING DATE: 1998-04-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2.
2 US-09-791-537-144266
0 US-09-647-978A-5
0 US-02-647-978A-5
0 US-02-22833A-13
0 PCT-US02-22833A-13
0 PCT-US02-22833A-13
0 PCT-US01-10-697-1551
2 US-00-012-697-1551
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0 US-00-791-537-23563
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US-09-757-781-1
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Matches 557; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Mouse
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US-09-647-978A-2
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                                                                                                                                                                                                                  October 9, 2003, 10:59:20 ; Search time 282.013 Seconds (without alignments) 1797.171 Million cell updates/sec
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1 MSDGTASARSSSPLDRDPAF......LSCAEESEEDCPRELTDPKS
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1: (cgn2 6/ptodata/1)/paa/PCTUS COMB.pep:*

2: (cgn2 6/ptodata/1)/paa/USO6 COMB.pep:*

3: (cgn2 6/ptodata/1)/paa/USO81 COMB.pep:*

5: (cgn2 6/ptodata/1)/paa/USO81 COMB.pep:*

6: (cgn2 6/ptodata/1)/paa/USO81 COMB.pep:*

7: (cgn2 6/ptodata/1)/paa/USO82 COMB.pep:*

6: (cgn2 6/ptodata/1)/paa/USO82 COMB.pep:*

7: (cgn2 6/ptodata/1)/paa/USO84 COMB.pep:*

10: (cgn2 6/ptodata/1)/paa/USO84 COMB.pep:*

10: (cgn2 6/ptodata/1)/paa/USO84 COMB.pep:*

11: (cgn2 6/ptodata/1)/paa/USO80 COMB.pep:*

12: (cgn2 6/ptodata/1)/paa/USO80 COMB.pep:*

13: (cgn2 6/ptodata/1)/paa/USO80 COMB.pep:*

14: (cgn2 6/ptodata/1)/paa/USO80 COMB.pep:*

15: (cgn2 6/ptodata/1)/paa/USO80 COMB.pep:*

16: (cgn2 6/ptodata/1)/paa/USO80 COMB.pep:*

17: (cgn2 6/ptodata/1)/paa/USO80 COMB.pep:*

18: (cgn2 6/ptodata/1)/paa/USO90 COMB.pep:*

19: (cgn2 6/ptodata/1)/paa/USO90 COMB.pep:*

10: (cgn2 6/ptodata/1)/paa/USO90 COMB.pep:*
                                 GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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CURRENT APPLICATION WUMBER: US/09/647,978A
CURRENT FILING DATE: 1090-10-06
PRIOR FILING DATE: 1999-04-19
PRIOR FILING DATE: 1999-04-19
PRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTION OF 2.2
SEQ ID NO 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 5, Application US/09647978A; GENERAL INFORMATION:
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ORGANISM: Human
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GENERAL INFORMATION:
APPLICANT: Bionomix. Inc.
APPLICANT: Benownix. Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261,210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SCOTEMBRE: Patentin version 3.0
SEQ ID NO 144266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TILLESKELVRSVRAILDMDCLPYGMEEAYTADGIKYFINHVTQTTSWIHPVMSAINLSC 540 [[[[[[[[[[[]]]]]]]]]]] TILLESKELVRSVRAILDMDCLPYGWEEAYTADGIKYFINHVTQTTSWIHPVMSAINLSC 540
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DGRLKRPGDQLVSINKESMIGVSFEEAKSIITRAKLRSESPWEIAFIRQKSYGGHPGNICC
                                                                                                                       PSPQVSEDCGPQTSTFTLLSSPSETLLPKTSSTPQTQDSTFPSCKAIQTKPEHDKTEHSP
                                                                                                                                                      PSPQVSEDCGPQTSTFTLLSSPSETLLPKTSSTPQTQDSTFPSCKAIQTKPEHDKTEHSP
                                                                                                                                                                                                    EALREQUQADSKGTVSFGDFVQVARSLFCLQLDEVNVGVHE1PSILDSQLLPCDSLEADE
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                                                              DGRLKPGDQLVSINKESMIGVSFERAKSIITRAKLRSESPWEIAFIRQKSYCGHPGNICC
                                                                                                                                                                                    ITSLONSPADTSNADIAPAWTDDDSGPQGKISLNPSVRLKAEKLEMALNYLGIQPTKEQR
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100.0%; Pred. No. 1.1e-207;
ive 0; Mismatches 0; 1
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Best Local Similarity 100.
Matches 557; Conservative
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61 DGRLKPGDQLVSVNKESMIGVSFEEAKSIITRAKLRLESAWEIAPIRQKSDNIQPENLSC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 AEAAQRQAHGMEMDYEEVIRLLEAEVSELKAQLADYSDQNKES 402
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 2187465CD1
PCT-US02-22833-13
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/314,798
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/316,639
PRIOR FILING DATE: 2001-08-31
PRIOR FILING DATE: 2001-08-31
PRIOR FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PERL Program
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application PC/TUS0222833A GENERAL INFORMATION:
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HONNCHELL, Cynthia D.
FORSYTHE, Ian J.
WALIA, Narinder K.
TANG, Y. Tom
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THANGAVELU, Kavitha
GIETZEN, Kimberly J.
AZIMZAI, Yalda
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DUGGAN, Brendan M.
TRAN, Bao
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BOROWSKY, Mark L.
BARROSO, Ines
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                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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PCT-US02-22833A-13
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                                          240 REALREQVQADSKGTVSFGDFVQVARSLFCLQLDEVNVGVHEIPSILDSQLLPCDSLEAD 299
                                                                                                                       EVCKLRQERNAALEERNVLKEKLLESEKHRKQLIEBLQNVKQEAKAVAEETRALRSRIHL 359
                                                                                                                                            178 PITS-ENSTVGLSNTDVASAWT-ENYGLQEKISLNPSVRFKAEKLEMALNYLGIQPTKEQ 235
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APPLICANT: LUCO, Wen
APPLICANT: LERR-MASON, PARTICIA M.
TITLE OF INVENTION: RECEPTORS AND MEMBRANE ASSOCIATED PROTEINS
FILE REFERENCE: PF-1082 PCT
CURRENT PELLING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: US 60/306,020
PRIOR PILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US 60/309,702
PRIOR PILING DATE: 2001-07-27
PRIOR PILING DATE: 2001-07-27
PRIOR PILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-10
PRIOR PLING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/311,718
PRIOR PLUNG DATE: 2001-08-10
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RICHARDSON, Thomas W.
ELLIOTT, Vicki S.
ZEBARJADIAN, Yeganeh
TRAN, Uyen K.
YAO, Monique G.
PETERSON, David P.
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HONNCHELL, Cynthia D.
FORSYTHE, Ian J.
WALIA, Narinder K.
TANG, Y. Tom
BOROMSKY, Mark L.
BAROSO, Ines
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THANGAVELU, Kavitha
GIETZEN, Kimberly J.
AZIMZAI, Yalda
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536 RSEENEEDCSRELPNQKS
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DUGGAN, Brendan M.
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BAUGHN, Mariah R.
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SMIGVSFEEAKSIITRAKLRSESPWEIAFIRQKSYCGHPGNICCPSPQVSEDCGPQTSTF 136
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APPLICANT: Garcia, Veronica
APPLICANT: Jones, Lee William
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: ISOLATED FROM HUMAN GENE EXPRESSION PRODUCTS
TITLE OF INVENTION: ISOLATED FROM HUMAN PROSTATE
FILE REFERENCE: 2300-16252
CURRENT APPLICATION NUMBER: PCT/US02/28214
CURRENT APPLICATION NUMBER: 60/254,648
PRIOR APPLICATION NUMBER: 60/254,648
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 60/254,648
PRIOR FILING DATE: 2000-13-13
NUMBER OF SEQ ID NOS: 1568
SOFTWARE: FastSEO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.1%; Score 1193; DB 1; Length 300;
51.8%; Pred. No. 2.1e-82;
tive 18; Mismatches 21; Indels 20
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                                                                                                                                      Sequence 1551, Application PC/TUS0228214 GENERAL INFORMATION:
                                                                                                                                                                                                                             Garcia, Pablo Dominguez
Kassam, Altaf
Lamson, George
Scott, Beth
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Crkvenjakov, Radomir
Dickson, Mark
Drmanac, Snezana
Labat, Ivan
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Best Local Similarity 51.8%
Matches 261; Conservative
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Kita, David
                                                                                                                                                                                                APPLICANT: Escobedo, Jaime APPLICANT: Garcia, Pablo I
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGRLKPGDQLVSINKESMIGVSFEEAKSIITRAKLRSESPWEIAFIRQKSYCGHPGNICC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DGRLKPGDQLVSVNKESMIGVSFEEAKSIITRAKLRLESAWEIAFIRQKSDNIQPENLSC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSDGTASARSSSPLDRDPAFRVITVTKETGLGLKILGGINRNEGPLVYIHEVIPGGDCYK
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                                                                                                                                                                                                         APPLICANT: LUO, WEN PARTICIA M.
TITLE OF INVENTION: RECEPTORS AND MEMBRANE ASSOCIATED PROTEINS FILE REPERENCE: PP-1082 PCT
CURRENT APPLICATION NUMBER: PCT/US02/22833A
CURRENT FILING DATE: 2002-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 47.5%; Score 1345; DB 1; Length 405; Best Local Similarity 69.5%; Pred. No. 7.3e-94; Matches 280; Conservative 37; Mismatches 58; Indelø 2
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OTHER INFORMATION: Incyte ID No: 2187465CD1
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2002-09-17
PRIOR FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US 60/306,020
PRIOR FILING DATE: 2001-07-27
PRIOR FILING DATE: 2001-07-27
PRIOR PRIOR DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-10
PRIOR PRIOR APPLICATION NUMBER: US 60/311,476
PRIOR APPLICATION NUMBER: US 60/311,718
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-14
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-18
PRIOR PRIOR FILING DATE: 2001-08-18
Joana X.
                   LI, Joana X.
RICHARDSON, Thomas W.
ELLIOTT, Vicki S.
ZEBARJADIAN, Yeganeh
                                                                                                                                         TRAN, Uyen K.
YAO, Monique G.
PETERSON, David P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT:
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APPLICANT: Ladunga, Steven
APPLICANT: Ladunga, Steven
APPLICANT: Spier, Eugene
APPLICANT: Rakin, Steven
APPLICANT: Rakin, Steven
APPLICANT: Rakin, Steven
APPLICANT: Rang, Yu
APPLICANT: BONAZZI, Vivien
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLOO0866
CURRENT APPLICATION NUMBER: US/60/236,804
CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 1071
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 455
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437 FIEALQEVLLDSSAPLSTLSERRAVLASQTSLPLLARNGRSFPATLLLESKELVRSVRAI 496
                                     -----SERRAVLASQTSLIPLGRNGRSIPATLALESKELVKSVRAL 276
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; Sequence 181, Application PC/TUSO147004
; GENERAL INFORMATION:
   APPLICANT: Hyseq, Inc
   TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-090
; CURRENT APPLICATION NUMBER: PCT/USO1/47004
; CURRENT APPLICATION NUMBER: 909/728,952
; PRIOR APPLICATION NUMBER: 09/728,952
; RICR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 181
                                                                                                                                            497 LDMDCLPYGWEEAYTADGIKYFIN 520
                                                                                                                                                                                             LDMDCLPYGWEEAYTADGIKYFIN 300
                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 455, Application US/60236804; GENERAL INFORMATION:
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224 DGTLDLVKY 232
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; ORGANISM: HUMAN
US-60-236-804-455
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US-60-236-804-455
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                                                                                                                                                                                                                                                                                                               APPLICANT: Garcia, Pablo Dominguez
APPLICANT: Garcia, Pablo Dominguez
APPLICANT: Kassam, Altaf
APPLICANT: Kassam, Altaf
APPLICANT: Scott, Beth
APPLICANT: Scott, Beth
APPLICANT: Dickson, Mark
APPLICANT: Leshkowitz, Dena
APPLICANT: Leshkowitz, Dena
APPLICANT: Leshkowitz, Dena
APPLICANT: Leshkowitz, Busin
APPLICANT: Stacke-Crain, Busin
APPLICANT: Stacke-Crain
APPLICANT: Sta
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                                                     277 LDMDCLPYGWEEAYTADGIKYFIN 300
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GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-10-012-697-1551
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CURRENT APPLICATION NUMBER: PCT/US01/01329
CURRENT FILING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 3506
SOFTHARE: PatentIn Ver. 2.0
SEQ ID NO 1354
LENGTH: 150
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ORGANISM: Homo sapiens
                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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US-09-764-891-3931
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                                                                                                  Length 217;
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20.3%; Score 574.5; DB 30; Length
al Similarity 59.8%; Pred. No. 3.4e-35;
122; Conservative 20; Mismatches 57; Indels
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-090
CURRENT APPLICATION NUMBER: US/10/416,991
CURRENT FILING DATE: 2003-05-16
PRIOR APPLICATION NUMBER: 09/728,952
                                                                                                  DB 1;
                                                                                                                  .4e-35;
                                                                                                  20.3%; Score 574.5; 159.8%; Pred. No. 3.4e ive 20; Mismatches
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10s-10-416-991-181
Sequence 181, Application US/10416991
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 181
LENGTH: 217
                                                                                                                  Best Local Similarity 59.8
Matches 122, Conservative
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ORGANISM: Homo sapiens
                        TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 122; Conserv
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      LENGTH: 217
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61 LFSSPPEILIPKTSSTPKTNNDILSSC---EIKTGYNKTVQIPITS-ENSTVGLSNTDVA 116
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids PCT-US01-01329-1354
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14.5%; Score 412; DB 1; Length 150;
Best Local Similarity 61.4%; Pred. No. 5.5e-23;
Matches 94; Conservative 14; Mismatches 39; Indels
                                                                                                 Query Match
14.5%; Score 412; DB 1; Length 150;
Best Local Similarity 61.4%; Pred. No. 5.5e-23;
Matches 94; Conservative 14; Mismatches 39; Indels
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TITLE OF INVENTION: Nucleic Acids, Froteins, and Antibodies FILE REFERENCE: PC006PCT
CURRENT APPLICATION NUMBER: PCT/US01/01339
CURRENT FILING DATE: 2001-03-17
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3931
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; Sequence 3931, Application PC/TUS0101339
; GENERAL INFORMATION:
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FEATURE
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LOCATION: (149)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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LOCATION: (149)

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-891-3931
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Best Local Similarity 61.4%; Pred. No. 5.5e-23;
Matches 94; Conservative 14; Mismatches 39; Indels
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APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT PILLIG DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER: OF SEQ ID NOS: 10231
SOFTWARE: Parentin Ver. 2.0
SEQ ID NO 3931
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA120C1
FILE REPLICATION NUMBER: US/10/080,090
CURRENT APPLICATION NUMBER: US/10/080,090
FIOT Application Femoved - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 3506
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1354
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61.4%; Pred. No. 5.5e-23;
tive 14; Mismatches 39;
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RESULT: 15

15.40-103-1354

15.6quence 1354, Application US/10205303

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9, 2003, 10:57:36; Search time 40.6459 Seconds (without alignments) 2175.142 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                       1107863 seqs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Murine syntaxin-4	Mouse syntaxin 4 i	Human syntaxin 4 i	Human novel polype	Human testicular a	Human reproductive	Human syntaxin 4 i	Novel human diagno	Novel human diagno
SUMMARIES 1D	AAY52446	AA015046	AA015047	ABG66753	ABB95970	AAM95273	AA015045	ABG03416	ABG10928
D3	21	23	23	23	22	22	23	22	22
* Query Match Length DB	557	557	554	217	150	150	72	549	1743
,	100.0	100.0	70.6	20.3	14.5	14.5	8.6	6.7	9.9
Score	2832	2832	2000.5	574.5	412	412	243	188.5	187.5
Result No.	-	7	Э	4	ហ	9	7	80	9

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ABG1228 AAY0724 ABJ2618 AAK6645 AAW2409	AAB19343 AAR71498 AAW75999 AAY90272 AAB60762 AAY5938			ABB6117; AAM4833; AAB4796; ABP7393; ABB1170 ABG0650
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ALIGN:MENTS

AAY52446 standard; protein; 557 AA.

AAY52446;

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Syntaxin-4 interacting protein; SYNIP; glucose; transport; GLUT4; vesicle translocation; insulin; regulation; SNARE; SNARE-like; soluble N-ethylmaleidide-sensitive factor attachment protein receptor; uptake; syntaxin-4; VAMP2; competition; binding; glucose storage; glucose utilisation; recombinant expression; gene therapy; diagnostic; antagonist; agonist; agonist; alprogen storage disease; obesity; type Ii; polycystic ovarian syndrome; hypotension; atherosclerosis; insulin resistance; antidiabetic; anorectic; hypotensive;
                                                                                                                                                                                                                                                                                                                219..264
/note= "Calcium-binding EF-hand domain"
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/note= "Tandem coiled coil domains"
                                                                   Murine syntaxin-4 interacting protein (SYNIP).
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/note= "WW domain"
                                       (first entry)
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16-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                              This sequence represents murine syntaxin-4 interacting protein (SYNIP), which is a novel insulin-regulated SNARE-like protein directly involved in the regulation of glucose transport and GLUT4 glucose transporter vesicle translocation. Insulin induces translocation of GLUT4 from the intracellular low density microsomal compartment to the cell surface, GLUT4 translocation playing an important role in the uptake of glucose intracellular low density microsomal compartment to the cell surface, GLUT4 translocation between the vesicle membrane SNARE of soluble N-ethylmaledide-sensitive factor attachment protein receptor), VAMP2, and the target membrane SNARE, syntaxin-4. SYNIPs competitively bind to syntaxin-4, preventing the ligand from interacting with its cognition incluses a dissociation of the SYNIP syntaxin-4 complex via a contract insulin receptor, and are only expressed in cells which exhibit insulin-responsive glucose transport and GLUT4 translocation. SYNIP proteins the binding affinity of SYNIP (syntaxin-4 complex via a corresponsive glucose transport and GLUT4 translocation. SYNIP proteins and on the binding affinity of syntaxin-4 complex via a card/or utilisation. SYNIP nucleotides may be used to recombinantly and/or utilisation. SYNIP proteins, in gene therapy, or as a source of diagnostic probes and primers. SYNIP proteins may be used to identify antagonists which will prevent the binding of SYNIP to syntaxin-4, thereby increasing transport may disease that may he translocation of identify antagonists which will prevent the hinding of SYNIP to syntaxin-4, thereby increasing transport may a source of diagnostic probes and primers. Which will be transport will accept that may he translocations and source of diagnostic transport may a source of diagnostic probes and primers which may be transport and contains the proteins and contains the proteins which will prevent the binding of SYNIP to very the syntaxin-4, thereby increasing the transpore transport and contains the proteins and the proteins and the pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: SYNIP cDNAs (mouse and human), and an additional SYNIP protein are also claimed, but the sequences are not given in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transport. The diseases that may be treated include diabetes (particularly type II), glycogen storage diseases, obesity, polycystic ovarian syndrome, hypertension, atherosclerosis and other diseases associated with insulin resistance.
                                                                                                                                                                                                                                                                                        Novel polypeptides and polymucleotides used for diagnosis of syndromes involving abnormal levels of glucose or abnormal GLUT4 translocation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ### WEDGTASARSSSPLDRDPAPRVITVTKETGLGLKILGGINRNEGPLVYIHEVIPGGDCYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGRLKPGDQLVSINKESMIGVSFEBAKSIITRAKLRSESPWEIAFIRQKSYCGHPGNICC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 PSPQVSEDCGPQTSTFTLLSSPSETLLPKTSSTPQTQDSTFPSCKAIQTKPEHDKTEHSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 ITSLDNSPADTSNADIAPAWTDDDSGPQGKISLNPSVRLKAEKLEMALNYLGIQPTKEQR
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100.0%; Pred. No. 1.9e-215;
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                                                                                                                                                                                                                Syu L;
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                                                                                                                                                   (WARN ) WARNER LAMBERT CO.
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Best Local Similarity 100.
Matches 557; Conservative
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WO9954465-A2
                                                                          19-APR-1999;
                                       28-OCT-1999.
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EALREQUOADSKGTVSFGDFVQVARSLFCLQLDEVNVGVHEIPSILDSQLLPCDSLEADE 300
                                             241 BALREQVQADSKGTVSFGDFVQVARSLFCLQLDEVNVGVFBIPSILDSQLLPCDSLBADE 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse, antisense gene therapy, Syntaxin 4 interacting protein, antisense oligonucleotide; diabetes; obesity; skeletal muscle disorder; inflammation; tumour formation.
                                                                                                                                                                                                                                            EMARKAPKASTERLIGETEAIQEVLLDSSAPLSTLSERRAVLASQTSLPLLARNGRSPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            T:LLESKELVRSVRAILDMDCLPYGWEEAYTAJGIKYFINHVTQTTSWIHPVMSALNLSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel antisense compound that hybridizes and inhibits nucleic acid molecule encoding Syntaxin 4 interacting protein, useful for treating diabetes, obesity and skeletal muscle disorder
                                                                                                                                                         301 VGKLRGERNAALEERNVLKEKLLESEKHRKQLIEELONVKGEAKAVAEETRALRSRIHLA
                                                                                                                                                                                                                EAAQRQAHGMEMDYEEVIRLLEAEVSELKAQLADYSDQNKESVQDLRKRVTVLDCQLRKS
                                                                                                                                                                                                                                                                                                                   EMARKAFKASTERLLGFIEAIQEVLLDSSAPLSTLSERRAVLASQTSLPLLARNGRSFPA
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                                                                                                         VGKLRQERNAAL EERNVLKEKLLESEKHRKQLI EELQNVKQEAKAVAEETRALRSRIHLA
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

October 9, 2003, 10:57:41; Search time 37.3649 Seconds (without alignments) 3819.179 Million cell updates/sec Run on:

US-09-647-978A-5 2784 1 MNKOYTSTVVSPSLLEKDPAF......LSRSEENEEDCSRELFNQKS 553 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

830525 segs, 258052604 residues

Searched:

830525 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_human:*
sp_mammal:*
sp_mhc:*; sp_unclassified: * sp_rodent:*
sp_virus:*
sp_vertebrate:* sp_organelle:*
sp_phage:*
sp_plant:* rvirus:* SPTREMBL 23:* 10: .. Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_bacteriap: *

sp archeap:*

SUMMARIES

Description	n[nosnm snm 68AM60		OBivz5 home sapien	Q14205 homo sapien	caenc	097961 vulpes vulp	095q64 caenorhabdi	095q66 caenorhabdi	P91146 caenorhabdi	096398 schistosoma	Q21022 caenorhabdi	Q22869 caenorhabdi	Ostew2 homo mapien	Q8tew3 homo sapien	Oginya drosophila	
ID	09WV89	Q8CFL1	527180	014205	019658	097961	095064	990560	P91146	096398	021022	022869	Q8TEW2	QUTEW3	QBINY8	QBMSD0
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* Query Match Length DB	557	533	245	3685	2003	1330	561	658	721	802	1133	2003	1319	1356	1652	1689
* Query Match	75.8	66.4	42.5	6.7	9.9	9.9	9.9	9.9	9.9	9.9	9.9	6.5	6.5	6.5	6.4	6.4
Score	2109	1848	1184	187.5	185	184	183	183	183	182.5	182.5	181	180	180	179.5	179.5
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6.4	6.4	6.4	6.4	6.3	•	6.3	•	6.2	6.2		6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	0.9	6.0	6.0	6.0	9.0	6.0	6.0	6.0	6.0	
179.5	179.5	179.5	7	175.5	175.5	175.5	175.5	172.5	171.5	171.5	171	169.5	169	169	169	169	169		168.5	168	167.5	167.5	167.5	167	166.5	166.5		166	
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Mus musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murihae; Mus.

NCBI_TaxID=10090;
     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Syntaxin4-interacting protein synip.
557 AA
PRT;
PRELIMINARY;
Q9WV89
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4

Gaps

9

75.8%; Score 2109; DB 11; Length 557; 76.5%; Pred. No. 6.5e-107; ive 49; Mismatches 76; Indels 6;

Best Local Similarity 76.5% Matches 427; Conservative

Similarity

Query Match

295

299

239

355

415

479

us-09-647-978a-5.rspt

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136 TLSLFSSPPEILIPKTSSTPKTNNDILSSCEIKTGYNKTVQIPITSENSTVGLSNTDVAS 195
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              121 PS-PQVSEDCGPQTSTFTLLSSPSETLLPKTSSTPQTQDSTPPSCKAIQTKPEH5KTEH5
                                                                                                            HQALRQQVQADSKGTVSFGDFVQVARNLFCLQLDEVNVGAHEISNILDSQLLPCDSSEAD
                                                                                                                           240 REALREQVQADSKGTVSFGDFVQVARSLFCLQLDEVNVGVHEIPSILDSQLLPCDSLEAD
                                                                                                                                                                                  AEAAQRQAHGMEMDYEEVIRLLSAKITSLKAQLADYSDQNKESVQDLKKRIMVLDCQLRK
                                                                                                                                                                                                                                          SEMARKTFEASTEKLLHFVEA1QEVFSONSTPLSNLSERRAVLASQTSLTPLGRNGRSIP
                                                                                                                                                                                                                                                                                             78 MIGVSFEEAKSIITRAKL - RLESAWEIAFIROKSDNIQPENLSCTSLIEASGEYGPQAS
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                                                                       EMERLKCERDDALKEVNTLKEKLLESDKQRKQLTEELQNVKQEAKAVVEETRALRSRIHL
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TSLIEASGEYGPQASTLSLFSSPPEILIPKTSSTFKTNNDILSSC---EIKTGYNKTVQI
                                                     PITS-ENSTVGLSNTDVASAWT-BNYGLQEKISLNPSVRFKAEKLEMALNYLGIQPTKEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                             081V25;
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC041485; ARH41485.1; -.
SEQUENCE 245 AA; 26974 MW; 4E92DDBBFD27DF79 CRC64;
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237; Conservative
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TISSUE=Eye;
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                                                      DGRLKPGDQLVSVNKESMIGVSFEEAKSIITRAKLRLESAWEIAFIRQKSDNIQPENLSC 120
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                                                                       AEAAQRQAHGMEMDYEEVIRLLEAKITELKAQLADYSDQNKESVQDLKKRIMVLDCQLRK
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC032881; AAH32881.1; -
SEQUENCE 533 AA; 58591 MW; 836BC19511E3AF09 CRC64;
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01-MAR-2003 (TYEMBLrel. 23, Created)
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01-MAR-2003 (TYEMBLrel. 23, Last annotes
Similar to syntaxin binding protein 4.
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379; Conservative
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Sequence 1359, A
Sequence 15590, A
Sequence 1136, Ap
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ITILE OF INVENTION: Gene Baccding Syntaxin Interacting Protein;
FILE REFERENCE: 09/647,978
CURRENT APPLICATION NUMBER: US/09/647,978
CURRENT APPLICATION NUMBER: PCT/US99/08568
FRIOR APPLICATION NUMBER: PCT/US99/08568
FRIOR FILING DATE: 1999-04-19
FRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VUMBER: 2.1
SEQ ID NO 5
IENGTH: 553
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20 US-09-647-978A-2
22 US-09-791-537-44266
1 PCT USO2-22833A-13
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26 US-09-791-537-44266
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27 USO2-22833A-13
28 US-10-16-991-181
29 US-10-16-991-181
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30 US-10-18-99331
30 US-10-18-676A-91389
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100.0%; Score 2784; DB 20;
Best Local Similarity 100.0%; Pred. No. 4.3e-200;
Matches 553; Conservative 0; Mismatches 0;
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US-09-647-978A-5
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2: (cqn2 6/ptodata/1/paa/USGG COMB.pep:*

3: (cgn2 6/ptodata/1/paa/USGG COMB.pep:*

5: (cgn2 6/ptodata/1/paa/USGB COMB.pep:*

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                                            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           553 20 US-09-647-978A-5
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Maximum Match 100%
Listing first 45 summaries
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540 CAEESEEDCPRELTDPKS 557
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) ORGANISM: Mus musculus
US-09-791-537-144266
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                                                                DGRLKPGDQLVSVNKESMIGVSFEEAKSIITRAKLRLESAWEIAPIRQKSDNIQPENLSC 120
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            KTFEASTEKLLHFVEAIQEVFSDNSTPLSNLSERRAVLASGTSLTPLGRNGRSIPATLAL
                                                                             181 SENSTVGLSNTDVASAWTENYGLOEKISLNPSVRFKAEKLEMALNYLGIOPTKEQHQALR
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APPLICANT: WATCHELL
APPLICANT: WATCHELL
TITLE OF INVENTION: Gene Encoding Syntaxin Interacting Protein
FILE REFERENCE: 09/647,978
CURRENT APPLICATION WHRER: US/09/647,978A
CURRENT FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/082,454
PRIOR APPLICATION NUMBER: 60/082,454
PRIOR FILING DATE: 1998-04-10
PRIOR FILING DATE: 1998-04-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Parentin Ver. 2.1
SEQ ID NO 2
LENTH: 557
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Best Local Similarity 76.54
Matches 427; Conservative
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ORGANISM: Mouse
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US-09-647-978A-2
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US-09-791-537-144266
Sequence 144266, Application US/09791537
Sequence 144266, Application US/09791537
Sequence 144266, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMP
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-202-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
                                    121 PS-PQVSEDCGPQTSTPTLLSSPSETLLPKTSSTPQTQDSTFPSCKALQTKPEHDKTEHS 179
                                                                                                                                                      240 REALREQVQADSKGTVSFGDFVQVARSLFCLQLDEVNVGVHEIPSILDSQLLFCDSLEAD 299
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                                                                                                                                                                                                                                              236 HQALRQQVQADSKGTVSFGDFVQVARNLFCLQLDEVNVGAHEISNILDSQLLPCDSSEAD 295
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Query Match
Best Local Similarity 100.
Matches 148; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                              October 9, 2003, 10:59:50 ; Search time 45.336 Seconds (without alignments) 1965.413 Million cell updates/sec
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1 MNKNTSTVVSPSLLEKDPAF......LSRSEENEEDCSRELPNQKS
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1: \( \can^2 \infty \) fordata\( \) Jubbpaa\( \) USO PUBCCMB.ppp: *

2: \( \can^2 \infty \) fordata\( \) Jubbpaa\( \) USO \( \) EW \( \) PUB.ppp: *

3: \( \can^2 \infty \) fordata\( \) Jubbpaa\( \) USO \( \) EW \( \) EWB. pep: *

4: \( \can^2 \infty \) fordata\( \) Jubbpaa\( \) USO \( \) EWB \( \) PUB. pep: *

5: \( \can^2 \infty \) fordata\( \) Jubbaa\( \) USO \( \) PUBCOMB.pep: *

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13: \( \can^2 \infty \) fordata\( \) Jubbaa\( \) USOB \( \) FUBCOMB.pep: *

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                                            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-757-781-62

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0 US-09-817-18-13240

2 US-10-128-714-3240

2 US-10-128-714-382

0 US-09-19-172-29

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Sequence 6, Appliance 1, Appliance 1, Appliance 1, Appliance 1, Appliance 2, Appliance 15, Appliance 15, Appliance 11, Appliance 12, Appliance 14, Appliance 16, A
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COCKTION: (149)
CHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
CS-09-764-891-3931
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Sequence 92,
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Publication No. US20030077808A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICANTON NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3931
LENGTH: 150
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100.0%; Pred. No. 3.3e-47;
tive 0; Mismatches 0; Indels
US-09-893-519A-73
US-10-197-666A-90
US-09-727-384-6
US-09-727-384-6
US-09-727-384-6
US-09-727-384-6
US-09-727-384-6
US-09-727-384-6
US-09-922-101-3
US-09-922-101-3
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US-09-922-101-3
US-09-922-101-3
US-09-921-407-3
US-09-921-407-3
US-09-921-407-3
US-09-921-407-3
US-09-921-407-3
US-09-921-407-3
US-09-971-101-3
US-09-971-101-3
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LENGTH: 1356
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US-09-757-781-1
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US-10-032-585-7646

US-10-032-585-7646

Sequence 7646, Application US/10032585

Publication No. US2033180953A1

SEGUENCE INFORMATION:

APPLICANT: Terry, Roemer D.

APPLICANT: Charles, Boone

APPLICANT: Howard, Bussey,

TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery,

TITLE OF INVENTION UNMER: US/10/032,585

CURRENT PILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 8000

SOFTWARE: Patentin version 3.1

LENGTH: 1881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----IEAS-GEYGPQASTLSLFSSPPEILI 148
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                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.8%; Score 190.5; DB 12; Length 1881; Best Local Similarity 21.2%; Pred. No. 6.7e-05; Matches 120; Conservative 100; Mismatches 183; Indels 163; Gaps
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                                                                                                                                                                                                                                                                                                                                  NAME/KEY: MISC_FEATURE
1_LOCATION: (1881)
1_OTHER INFORMATION: X=any amino acid
US-10-032-585-7646
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ORGANISM: Candida albicans
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588 ----TFEVPL-NDSGSAGLGVSVKGNRSKENHADLGIFVKSIINGGAASKDGRLRVNDQL
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6.5%; Score 180; DB 10; Length 1356;
Best Local Similarity 21.6%; Pred. No. 0.00024;
Matches 116; Conservative 97; Mismatches 186; Indels 138;
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OTHER INFORMATION: Incyte ID No. US20020137166A: 2582063CD1
                                                                                                               GENERAL INCORMATION:
APPLICANT: Reddy, Roopa
APPLICANT: Reddy, Roopa
APPLICANT: Baughn, Mariah R.
APPLICANT: Baughn, Mariah R.
APPLICANT: Krasnow, Randi E.
TITLE OF INVENTION: ASIP-RELATED PROTEINS
FILE REFERENCE: PC-0032 US
CURRENT APPLICATION NUMBER: US/09/757,781
CURRENT FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 63
SEQ ID NO 2
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Patent No. US20020137166A1
GENERAL INFORMATION:
APPLICANT: Reddy, Roopa
APPLICANT: Tang, Y. Tom
APPLICANT: Baughn, Mariah R.
APPLICANT: Krasnow, Randi E.
Sequence 2, Application US/09757781
Patent No. US20020137166A1
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Tang, Y. Tom
Baughn, Mariah R.
Krasnow, Randi E.
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ORGANISM: Homo sapiens
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31, Appl 4, Appli 4, Appli 4, Appli 12, Appli 12, Appl 3944, Ap 16965, A 4, Appli 4, Appli

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APPLICANT: RATTNER, JEROME B.

TITLE OF INVENTION: NUCLEIC ACID ENCODING A
TITLE OF INVENTION: TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN,
TITLE OF INVENTION: AND METHODS OF USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: DANN, DORFMAN, HERRELL AND SKILLMAN
                      Sequence
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ZIP: 19103-2307

ZIP: 19103-2307

COMPUTER ENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAILE
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/33,700
FILING DATE: 09-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REBD, JANET E.
REGIGTRATION: 1875
TELEPRONE: (215) 563-4106
TELEPRONE: (215) 563-4104
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TENDAMATICS: TENDAMATICS:
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                                                                                                                                                                                                                                                                                                        US-09-107-532A-3944
US-09-252-991A-16965
US-08-951-912-4
US-09-174-077-4
                                                            US-09-306-998-3

US-09-562-737-22

US-09-562-737-21

PCT-US93-03077-1

US-09-59-6848-31

US-08-68-095-737-4

US-08-480-145-4

US-08-968-751-4

US-08-968-751-4

US-08-968-751-4
                                           US-09-914-259-11
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STRANDEDNESS: sir
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ANTI-SENSE: NO
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Sequence 5080, Ap
                                                                                                                                                          ; Search time 14.9459 Seconds (without alignments) 1565.502 Million cell updates/sec
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Sequence 2, Al
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/cgn2 6/ptcdata/1/iaa/5B COMB.pep:*
/cgn2 6/ptcdata/1/iaa/6A COMB.pep:*
/cgn2 6/ptcdata/1/iaa/6B COMB.pep:*
/cgn2 6/ptcdata/1/iaa/PCTUS COMB.pep:*
/cgn2 6/ptcdata/1/iaa/PCTUS COMB.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-353-700-1
US-08-39-16216-1
US-08-290-640-46
US-09-290-640-3
US-09-100-804-3
US-09-1010-804-3
US-09-1010-804-3
US-09-1010-804-3
US-09-1010-804-3
US-09-101-801B-10
US-09-101-81B-10
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US-09-101-821B-4
US-09-101-821B-4
US-09-101-821B-4
US-09-101-821B-4
US-09-157-420-1
US-09-157-420-1
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US-09-123-262-2
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US-09-123-282-2
US-09-123-820-2
US-09-11-83-2
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    425 ASTEKLLHFVEAIQEVFSDNST---PLSNLSERRAVLASQTSLTPL-GRNGRSIPATLAL
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Patent No. 5710022
GENERAL INFORMATION:
APPLICANT: Zhu, Xueliang
APPLICANT: Zhu, Xueliang
APPLICANT: Lee, Wen-Hwa
TITLE OF INVENTION: A No. 5710022el Nuclear Mitotic Phosphoprotein
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                     6.7%; Score 186; DB 5; Length 3248;
21.6%; Pred. No. 3.9e-06;
Live 80; Mismatches 180; Indels 118;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PARENTER RELEGION RELEGION
TOTRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/128,254
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STREET: 4370 La Jolla Village Drive, Suite 700
                  TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOJECULE TYPE: protein
3248 amino acids
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Matches 104; Conservative
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STATE: California
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PCT-US95-16216-1
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US-08-328-254-6
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                                        1920 ACIELEKIVGELKKENSDLSEKLEYFSCDHQELLQRVETSEGLNSDLEMHAD----- 1971
                                                                                                                          1972 -----KSSREDIGDNVAKVNDSWKERFLDVENELSRIRSEKASIEHEALYLEADLEVVQT 2026
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                                                                                                                                                                                                                                                       314 LKEKL.--LESDKORKOLTE-ELON----VKOEAKAVVEETRALRSRIHLAEAAQRQAHGM 366
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SCTSLIEASGEYGPQASTLS----LFSSPPEILIPKTSSTPKTNNDILSSCEIKTGYNKT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Yen, Timothy J.
APPLICANT: Rattner, Jerome B.
TITLE OF INVENTION: Nucleic Acid Encoding a Transiently
TITLE OF INVENTION: Expressed Kinetochore Protein, and Methods of Use
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
                                                                                                                                                                     230 QP-----TKEQHQALRQQVQADSKGTVSFGDFVQVARN---
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                                                                                    175 VQIPITSENSTVGLSNTDVASAWTENY-----GLQEKISLNPSVRPKAEKLEMALNYLGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DAIL:
CLASIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,700
FILING DATE: 09-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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October 9, 2003, 10:57:36 ; Search time 40.3541 Seconds (without alignments) 2175.142 Million cell updates/sec
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2784
1 MNKATSTVVSPSLLEKDPAF......LSRSEENEEDCSRELPNQKS 553
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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			Description		Human syntaxin 4 i	Murine syntaxin-4	Mouse syntaxin 4 i	Human novel polyne	Human testicular a	Human reproductive	Novel human diagno	Novel human diagno	Human syntaxin 4 i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression of Syntaxin 4 interacting protein. The antisense oligonucleotides of the invention are useful for inhibiting the expression of Syntaxin 4 interacting protein in cells or tissues. The antisense oligonucleotides are also useful for treating an animal having a disease or condition associated with Syntaxin 4 interacting protein (e.g. diabetes, obesity or a skeletal muscle disorder). The antisense oligonucleotides can also be used to prevent or delay infection, inflammation and tumour formation. The present amino acid sequence represents a human Syntaxin 4 interacting protein.
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                                                        invention comprises antisense oligonucleotides designed to inhibit
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encoding Syntaxin 4 interacting protein, useful for treating , obesity and skeletal muscle disorder
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                               Disclosure; Page 100-104; 154pp; English
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This sequence represents murine syntaxin-4 interacting protein (SYNIP), which is a novel insulin-regulated SNARE-like protein directly involved in the regulation of glucose transporter and GLUT4 glucose transporter vesicle translocation. Insulin induces translocation of GLUT4 from the intracellular low density microsomal compartment to the Cell's urface, GLUT4 translocation playing an important role in the uptake of glucose contains the uptake of glucose by cells. Insulin-stimulated glucose transport and GLUT4 translocation require specific interactions between the vesicle membrane SNARE (Soluble Nethylmaleidide-sensitive factor attachment protein receptor), WAMP2, and the target membrane SNARE, syntaxin-4. SYNIPs competitively bind to syntaxin-4, preventing the ligand from interacting which text compate intracellular receptor, and are only expressed in cells which exhibit insulin-responsive glucose transport and GLUT4 translocation.

CC finsulin induces a dissociation of the SYNIPsyntaxin-4 complex via a decrease in the binding affinity of SYNIP for syntaxin-4. Binding of the SYNIP Cterminal domain is in contrast refractive to insulin stimulation. But minibite splucose transport and GLUT4 translocation. SYNIP proteins on an uncleotides may be used in translocation or abnormal glucose storage characterised by abnormal GLUT4 translocation or abnormal glucose storage express SYNIP proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           express SYMIP proteins, in gene therapy, or as a source of diagnostic probes and primers. SYNIP proteins may be used to identify antagonists which will prevent the binding of SYNIP to syntaxin-4, thereby increasing glucose transport, or agonists, which will act to decrease glucose transport. The diseases that may be treated include diabetes transport. The diseases that may be treated include diabetes ovarian syndrome, hypertension, atherosclerosis and other diseases associated with insulin resistance.
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                                          vesicle translocation; insulin; regulation; SNARE; SNARE-like; soluble N-ethylmataladide-sensitive factor attachment protein receptor; uptake; syntaxin-4; VAMPE; competition; binding; glucose storage; glucose utilisation; recombinant expression; gene therapy; diagnostic; antagonist; agonist; diabetes; glycogen storage disease; obesity; type II; polycystic ovarian syndrome; hypertension; atherosclerosis; insulin resistance; antidiabetic; anorectic; hypotensive;
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involving abnormal levels of glucose or abnormal GLUT4 translocation
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transport; GLUT4;
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interacting protein; SYNIP; glucose;
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